> This Raw Listing contains the General Information
> Section and up to first 5 pages.

```
 1    <110> APPLICANT: Tavtigian, Sean V.
 2          Teng, David H.F.
 3          Simard, Jacques
 4          Rommens, Johanna M.
 5          Myriad Genetics, Inc.
 6    <120> TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
 7          Gene and a Paralog and Orthologous Genes
 8    <130> FILE REFERENCE: 2318-258
 9    <140> CURRENT APPLICATION NUMBER: US/09/988,687
10    <141> CURRENT FILING DATE: 2001-11-20
11    <150> EARLIER APPLICATION NUMBER: 09/564,805
12    <151> EARLIER FILING DATE: 2000-05-05
13    <150> EARLIER APPLICATION NUMBER: US 60/107,468
14    <151> EARLIER FILING DATE: 1998-11-06
15    <150> EARLIER APPLICATION NUMBER: 09/434,382
16    <151> EARLIER FILING DATE: 1999-11-05
17    <160> NUMBER OF SEQ ID NOS: 240
18    <170> SOFTWARE: PatentIn Ver. 2.0
19    <210> SEQ ID NO 1
20    <211> LENGTH: 2481
21    <212> TYPE: DNA
22    <213> ORGANISM: Homo sapiens
23    <220> FEATURE:
24    <221> NAME/KEY: CDS
25    <222> LOCATION: (1)..(2478)
26    <400> SEQUENCE: 1
27          atg tgg gcg ctt tgc tcg ctg ctg cgg tcc gcg gcc gga cgc acc atg      48
28          Met Trp Ala Leu Cys Ser Leu Leu Arg Ser Ala Ala Gly Arg Thr Met
29           1               5                  10                  15
30          tcg cag gga cgc acc ata tcg cag gca ccc gcc cgc cgc gag cgg ccg      96
31          Ser Gln Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro
32                          20                  25                  30
33          cgc aag gac ccg ctg cgg cac ctg cgc acg cga gag aag cgc gga ccg     144
34          Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
35                      35                  40                  45
36          tcg ggg tgc tcc ggc ggc cca aac acc gtg tac ctg cag gtg gtg gca     192
37          Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
38                   50                  55                  60
39          gcg ggt agc cgg gac tcg ggc gcc gcg ctc tac gtc ttc tcc gag ttc     240
40          Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
41                   65                  70                  75                  80
42          aac cgg tat ctc ttc aac tgt gga gaa ggc gtt cag aga ctc atg cag     288
43          Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Val Gln Arg Leu Met Gln
44                          85                  90                  95
```

ENTERED

```
45      gag cac aag tta aag gtt gct cgc ctg gac aac ata ttc ctg aca cga    336
46      Glu His Lys Leu Lys Val Ala Arg Leu Asp Asn Ile Phe Leu Thr Arg
47              100                     105                     110
48      atg cac tgg tct aat gtt ggg ggc tta agt gga atg att ctt act tta    384
49      Met His Trp Ser Asn Val Gly Gly Leu Ser Gly Met Ile Leu Thr Leu
50              115                     120                     125
51      aag gaa acc ggg ctt cca aag tgt gta ctt tct gga cct cca caa ctg    432
52      Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu
53              130                     135                     140
54      gaa aaa tac ctc gaa gca atc aaa ata ttt tct ggt cca ttg aaa gga    480
55      Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly
56      145                     150                     155                160
57      ata gaa ctg gct gtg cgg ccc cac tct gcc cca gaa tac gag gat gaa    528
58      Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu
59                      165                     170                     175
60      acc atg aca gtt tac cag atc ccc ata cac agt gaa cag agg agg gga    576
61      Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly
62                      180                     185                     190
63      aag cac caa cca tgg cag agt cca gaa agg cct ctc agc agg ctc agt    624
64      Lys His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser
65              195                     200                     205
66      cca gag cga tct tca gac tcc gag tcg aat gaa aat gag cca cac ctt    672
67      Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu
68              210                     215                     220
69      cca cat ggt gtt agc cag aga aga ggg gtc agg gac tct tcc ctg gtc    720
70      Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val
71      225                     230                     235                240
72      gta gct ttc atc tgt aag ctt cac tta aag aga gga aac ttc ttg gtg    768
73      Val Ala Phe Ile Cys Lys Leu His Leu Lys Arg Gly Asn Phe Leu Val
74                      245                     250                     255
75      ctc aaa gca aag gag atg ggc ctc cca gtt ggg aca gct gcc atc gct    816
76      Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala
77              260                     265                     270
78      ccc atc att gct gct gtc aag gac ggg aaa agc atc act cat gaa gga    864
79      Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly
80              275                     280                     285
81      aga gag att ttg gct gaa gag ctg tgt act cct cca gat cct ggt gct    912
82      Arg Glu Ile Leu Ala Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala
83              290                     295                     300
84      gct ttt gtg gtg gta gaa tgt cca gat gaa agc ttc att caa ccc atc    960
85      Ala Phe Val Val Val Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile
86      305                     310                     315                320
87      tgt gag aat gcc acc ttt cag agg tac caa gga aag gca gat gcc ccc    1008
88      Cys Glu Asn Ala Thr Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro
89                      325                     330                     335
90      gtg gcc ttg gtg gtt cac atg gcc cca gca tct gtg ctt gtg gac agc    1056
91      Val Ala Leu Val Val His Met Ala Pro Ala Ser Val Leu Val Asp Ser
92                      340                     345                     350
93      agg tac cag cag tgg atg gag agg ttt ggg cct gac acc cag cac ttg    1104
94      Arg Tyr Gln Gln Trp Met Glu Arg Phe Gly Pro Asp Thr Gln His Leu
```

```
 95                    355                   360                   365
 96        gtc ctg aat gag aac tgt gcc tca gtt cac aac ctt cgc agc cac aag    1152
 97        Val Leu Asn Glu Asn Cys Ala Ser Val His Asn Leu Arg Ser His Lys
 98                    370                   375                   380
 99        att caa acc cag ctc aac ctc atc cac ccg gac atc ttc ccc ctg ctc    1200
100        Ile Gln Thr Gln Leu Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu
101        385                   390                   395                   400
102        acc agt ttc cgc tgt aag aag gag ggc ccc acc ctc agt gtg ccc atg    1248
103        Thr Ser Phe Arg Cys Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met
104                            405                   410                   415
105        gtt cag ggt gaa tgc ctc ctc aag tac cag ctc cgt ccc agg agg gag    1296
106        Val Gln Gly Glu Cys Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu
107                    420                   425                   430
108        tgg cag agg gat gcc att att act tgc aat cct gag gaa ttc ata gtt    1344
109        Trp Gln Arg Asp Ala Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Val
110                    435                   440                   445
111        gag gcg ctg cag ctt ccc aac ttc cag cag agc gtg cag gag tac agg    1392
112        Glu Ala Leu Gln Leu Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg
113                    450                   455                   460
114        agg agt gcg cag gac ggc cca gcc cca gca gag aaa aga agt cag tac    1440
115        Arg Ser Ala Gln Asp Gly Pro Ala Pro Ala Glu Lys Arg Ser Gln Tyr
116        465                   470                   475                   480
117        cca gaa atc atc ttc ctt gga aca ggg tct gcc atc ccg atg aag att    1488
118        Pro Glu Ile Ile Phe Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile
119                            485                   490                   495
120        cga aat gtc agt gcc aca ctt gtc aac ata agc ccc gac acg tct ctg    1536
121        Arg Asn Val Ser Ala Thr Leu Val Asn Ile Ser Pro Asp Thr Ser Leu
122                    500                   505                   510
123        cta ctg gac tgt ggt gag ggc aca ttt ggg cag ctg tgc cgt cat tac    1584
124        Leu Leu Asp Cys Gly Glu Gly Thr Phe Gly Gln Leu Cys Arg His Tyr
125                    515                   520                   525
126        gga gac cag gtg gac agg gtc ctg ggc acc ctg gct gct gtg ttt gtg    1632
127        Gly Asp Gln Val Asp Arg Val Leu Gly Thr Leu Ala Ala Val Phe Val
128                    530                   535                   540
129        tcc cac ctg cac gca gat cac cac acg ggc ttg cca agt atc ttg ctg    1680
130        Ser His Leu His Ala Asp His His Thr Gly Leu Pro Ser Ile Leu Leu
131        545                   550                   555                   560
132        cag aga gaa cgc gcc ttg gca tct ttg gga aag ccg ctt cac cct ttg    1728
133        Gln Arg Glu Arg Ala Leu Ala Ser Leu Gly Lys Pro Leu His Pro Leu
134                    565                   570                   575
135        ctg gtg gtt gcc ccc aac cag ctc aaa gcc tgg ctc cag cag tac cac    1776
136        Leu Val Val Ala Pro Asn Gln Leu Lys Ala Trp Leu Gln Gln Tyr His
137                    580                   585                   590
138        aac cag tgc cag gag gtc ctg cac cac atc agt atg att cct gcc aaa    1824
139        Asn Gln Cys Gln Glu Val Leu His His Ile Ser Met Ile Pro Ala Lys
140                    595                   600                   605
141        tgc ctt cag gaa ggg gct gag atc tcc agt cct gca gtg gaa aga ttg    1872
142        Cys Leu Gln Glu Gly Ala Glu Ile Ser Ser Pro Ala Val Glu Arg Leu
143                    610                   615                   620
144        atc agt tcg ctg ttg cga aca tgt gat ttg gaa gag ttt cag acc tgt    1920
```

```
145        Ile Ser Ser Leu Leu Arg Thr Cys Asp Leu Glu Glu Phe Gln Thr Cys
146        625                 630                 635                 640
147        ctg gtg cgg cac tgc aag cat gcg ttt ggc tgt gcg ctg gtg cac acc        1968
148        Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu Val His Thr
149                        645             650                 655
150        tct ggc tgg aaa gtg gtc tat tcc ggg gac acc atg ccc tgc gag gct        2016
151        Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro Cys Glu Ala
152                        660                 665                 670
153        ctg gtc cgg atg ggg aaa gat gcc acc ctc ctg ata cat gaa gcc acc        2064
154        Leu Val Arg Met Gly Lys Asp Ala Thr Leu Leu Ile His Glu Ala Thr
155                675                 680                 685
156        ctg gaa gat ggt ttg gaa gag gaa gca gtg gaa aag aca cac agc aca        2112
157        Leu Glu Asp Gly Leu Glu Glu Glu Ala Val Glu Lys Thr His Ser Thr
158            690                 695                 700
159        acg tcc caa gcc atc agc gtg ggg atg cgg atg aac gcg gag ttc att        2160
160        Thr Ser Gln Ala Ile Ser Val Gly Met Arg Met Asn Ala Glu Phe Ile
161        705                 710                 715                 720
162        atg ctg aac cac ttc agc cag cgc tat gcc aag gtc ccc ctc ttc agc        2208
163        Met Leu Asn His Phe Ser Gln Arg Tyr Ala Lys Val Pro Leu Phe Ser
164                        725                 730                 735
165        ccc aac ttc agc gag aaa gtg gga gtt gcc ttt gac cac atg aag gtc        2256
166        Pro Asn Phe Ser Glu Lys Val Gly Val Ala Phe Asp His Met Lys Val
167                        740                 745                 750
168        tgc ttt gga gac ttt cca aca atg ccc aag ctg att ccc cca ctg aaa        2304
169        Cys Phe Gly Asp Phe Pro Thr Met Pro Lys Leu Ile Pro Pro Leu Lys
170                755                 760                 765
171        gcc ctg ttt gct ggc gac atc gag gag atg gag gag cgc agg gag aag        2352
172        Ala Leu Phe Ala Gly Asp Ile Glu Glu Met Glu Glu Arg Arg Glu Lys
173            770                 775                 780
174        cgg gag ctg cgg cag gtg cgg gcg gcc ctc ctg tcc agg gag ctg gca        2400
175        Arg Glu Leu Arg Gln Val Arg Ala Ala Leu Leu Ser Arg Glu Leu Ala
176        785                 790                 795                 800
177        ggc ggc ctg gag gat ggg gag cct cag cag aag cgg gcc cac aca gag        2448
178        Gly Gly Leu Glu Asp Gly Glu Pro Gln Gln Lys Arg Ala His Thr Glu
179                        805                 810                 815
180        gag cca cag gcc aag aag gtc aga gcc cag tga                            2481
181        Glu Pro Gln Ala Lys Lys Val Arg Ala Gln
182                        820                 825
183   <210> SEQ ID NO 2
184   <211> LENGTH: 826
185   <212> TYPE: PRT
186   <213> ORGANISM: Homo sapiens
187   <400> SEQUENCE: 2
188        Met Trp Ala Leu Cys Ser Leu Leu Arg Ser Ala Ala Gly Arg Thr Met
189        1                 5                   10                  15
190        Ser Gln Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro
191                        20                  25                  30
192        Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
193                    35                  40                  45
194        Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
```

195	50 55 60
196	Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
197	65 70 75 80
198	Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Val Gln Arg Leu Met Gln
199	85 90 95
200	Glu His Lys Leu Lys Val Ala Arg Leu Asp Asn Ile Phe Leu Thr Arg
201	100 105 110
202	Met His Trp Ser Asn Val Gly Gly Leu Ser Gly Met Ile Leu Thr Leu
203	115 120 125
204	Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu
205	130 135 140
206	Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly
207	145 150 155 160
208	Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu
209	165 170 175
210	Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly
211	180 185 190
212	Lys His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser
213	195 200 205
214	Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu
215	210 215 220
216	Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val
217	225 230 235 240
218	Val Ala Phe Ile Cys Lys Leu His Leu Lys Arg Gly Asn Phe Leu Val
219	245 250 255
220	Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala
221	260 265 270
222	Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly
223	275 280 285
224	Arg Glu Ile Leu Ala Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala
225	290 295 300
226	Ala Phe Val Val Val Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile
227	305 310 315 320
228	Cys Glu Asn Ala Thr Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro
229	325 330 335
230	Val Ala Leu Val Val His Met Ala Pro Ala Ser Val Leu Val Asp Ser
231	340 345 350
232	Arg Tyr Gln Gln Trp Met Glu Arg Phe Gly Pro Asp Thr Gln His Leu
233	355 360 365
234	Val Leu Asn Glu Asn Cys Ala Ser Val His Asn Leu Arg Ser His Lys
235	370 375 380
236	Ile Gln Thr Gln Leu Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu
237	385 390 395 400
238	Thr Ser Phe Arg Cys Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met
239	405 410 415
240	Val Gln Gly Glu Cys Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu
241	420 425 430
242	Trp Gln Arg Asp Ala Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Val
243	435 440 445
244	Glu Ala Leu Gln Leu Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg

Line	?	Error/Warning	Original Text
881	W	"N" or "Xaa" used: Feature required	agcatcactc atgaaggaag agaggtgaga tgcctggt
1113	W	"N" or "Xaa" used: Feature required	caggaattca gcacatactc attgttcagn n
1335	W	"N" or "Xaa" used: Feature required	caggaattca gcacatactc attgttcagn n
2308	W	"N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa His Xaa His Xaa Asp His X
2319	W	"N" or "Xaa" used: Feature required	tttaatacga ctcactatag ggaatttggc cctcgagn
2443	W	"N" or "Xaa" used: Feature required	tttaatacga ctcactatag ggaatttggc cctcgagn
2703	W	"N" or "Xaa" used: Feature required	gaa gcc act ctg gag gat cnc ttg gaa gag g
2709	W	"N" or "Xaa" used: Feature required	gag ttc atc atg ctg aac cac ttc agt cag c
2715	W	"N" or "Xaa" used: Feature required	atg aag gtc tgn ttt gga gac ttc ccg aca g
2822	W	"N" or "Xaa" used: Feature required	Glu Ala Thr Leu Glu Asp Xaa Leu Glu Glu G
2826	W	"N" or "Xaa" used: Feature required	Glu Phe Ile Met Leu Asn His Phe Ser Gln A
2830	W	"N" or "Xaa" used: Feature required	Met Lys Val Xaa Phe Gly Asp Phe Pro Thr V